RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _/0/663,650_

Source: _1FWO_

Date Processed by STIC: _7/1/04_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand-Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

IFWO

RAW SEQUENCE LISTING   DATE: 07/06/2004
PATENT APPLICATION: US/10/663,650   TIME: 15:31:23

Input Set : A:\US-972-Sequence.txt
Output Set: N:\CRF4\07062004\J663650.raw

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   3 <110> APPLICANT: Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo
W-->  4 <120> TITLE OF INVENTION: Trehalose receptor and method for detecting trehalose with
the same
C-->  5 <140> CURRENT APPLICATION NUMBER: US/10/663,650
C-->  5 <141> CURRENT FILING DATE: 2003-09-17
W-->  0 <130> FILE REFERENCE:
W-->  5 <160> NUMBER OF SEQ ID: 24
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error throughout

ERRORED SEQUENCES

see p.3, too

Does Not Comply
Corrected Diskette Needed

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   357 <210> SEQ ID NO: 6
   358 <211> LENGTH: 1353
   359 <212> TYPE: DNA
   360 <213> ORGANISM: Mus musculus
   362 <300> PUBLICATION INFORMATION:
   363 <308> DATABASE ACCESSION NO: GENBANK M80632
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   369 Met Ala Arg Ser Leu Thr Trp Gly Cys Cys Pro Trp Cys Leu Thr Glu
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   378 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
   379     50                  55                  60
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   381 Ile His Gly Val Gly Tyr Ser Glu Glu Asp Arg Arg Ala Phe Arg Leu
   382 65                  70                  75                  80
   383 ctc atc tac cag aac atc ttc gtc tcc atg cag gcc atg ata gat gcg 330
   384 Leu Ile Tyr Gln Asn Ile Phe Val Ser Met Gln Ala Met Ile Asp Ala
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   387 Met Asp Arg Leu Gln Ile Pro Phe Ser Arg Pro Asp Ser Lys Gln His
   388             100                 105                 110
   389 gcc agc cta gtg atg acc cag gac ccc tat aaa gtg agc aca ttc gag 426
   390 Ala Ser Leu Val Met Thr Gln Asp Pro Tyr Lys Val Ser Thr Phe Glu
   391         115                 120                 125
   392 aag cca tat gca gtg gcc atg cag tac ctg tgg cgg gac gcg ggc atc 474
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insert <309> and response

Wherever <308> has a response, insert <309> and response. Mandatory.

<309> line lists the Database Entry Date

This error also appears in Sequences 1 through 3, too.

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393 Lys Pro Tyr Ala Val Ala Met Gln Tyr Leu Trp Arg Asp Ala Gly Ile
394     130                 135                 140
395 cgt gca tgc tac gag cga agg cgt gaa ttc cac ctt ctg gac tcc gcg 522
396 Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
397 145                 150                 155                 160
398 gtg tat tac ctg tca cac ctg gag cgc ata tca gag gac agc tac atc 570
399 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Ser Glu Asp Ser Tyr Ile
400                     165                 170                 175
401 ccc act gcg caa gac gtg ctg cgc agt cgc atg ccc acc aca ggc atc 618
402 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
403                     180                 185                 190
404 aat gag tac tgc ttc tcc gtg aag aaa acc aaa ctg cgc atc gtg gat 666
405 Asn Glu Tyr Cys Phe Ser Val Lys Lys Thr Lys Leu Arg Ile Val Asp
406             195                 200                 205
407 gtt ggt ggc cag agg tca gag cgt agg aaa tgg att cac tgt ttc gag 714
408 Val Gly Gly Gln Arg Ser Glu Arg Arg Lys Trp Ile His Cys Phe Glu
409     210                 215                 220
410 aac gtg att gcc ctc atc tac ctg gcc tcc ctg agc gag tat gac cag 762
411 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
412 225                 230                 235                 240
413 tgc cta gag gag aac gat cag gag aac cgc atg gag gag agt ctc gct 810
414 Cys Leu Glu Glu Asn Asp Gln Glu Asn Arg Met Glu Glu Ser Leu Ala
415                     245                 250                 255
416 ctg ttc agc acg atc cta gag ctg ccc tgg ttc aag agc acc tcg gtc 858
417 Leu Phe Ser Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
418                     260                 265                 270
419 atc ctc ttc ctc aac aag acg gac atc ctg gaa gat aag att cac acc 906
420 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Asp Lys Ile His Thr
421             275                 280                 285
422 tcc cac ctg gcc aca tac ttc ccc agc ttc cag gga ccc cgg cga gac 954
423 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Arg Arg Asp
424     290                 295                 300
425 gca gag gcc gcc aag agc ttc atc ttg gac atg tat gcg cgc gtg tac 1002
426 Ala Glu Ala Ala Lys Ser Phe Ile Leu Asp Met Tyr Ala Arg Val Tyr
427 305                 310                 315                 320
428 gcg agc tgc gca gag ccc cag gac ggt ggc agg aaa ggc tcc cgc gcg 1050
429 Ala Ser Cys Ala Glu Pro Gln Asp Gly Gly Arg Lys Gly Ser Arg Ala
430                     325                 330                 335
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432 Arg Arg Phe Phe Ala His Phe Thr Cys Ala Thr Asp Thr Gln Ser Val
433                     340                 345                 350
434 cgc agc gtg ttc aag gac gtg cgg gac tcg gtg ctg gcc cgg tac ctg 1146
435 Arg Ser Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
436             355                 360                 365
437 gac gag atc aac ctg ctg 1164
438 Asp Glu Ile Asn Leu Leu
439     370
440 tgacgcggga cagggaaccc caagcgcgac gcgtcgtggc gaggacatac ctcccctgg 1224
441 tggccgcgcg tggaactgca ggtccaggag ctgccaagtg gggaagccag cccacaggag 1284
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RAW SEQUENCE LISTING   DATE: 07/06/2004
PATENT APPLICATION: US/10/663,650   TIME: 15:31:23

Input Set : A:\US-972-Sequence.txt
Output Set: N:\CRF4\07062004\J663650.raw

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      447 <212> TYPE: DNA
      448 <213> ORGANISM: Artificial Sequence
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W--> 450 <223> OTHER INFORMATION:
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      453 <210> SEQ ID NO: 8
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      472 tgcccggagc cctctccagg gccggctggg ctgggggttg ccctggccag caggggcccg 180
      473 ggggcgatgc cacccggtgc cgactgaggc caccgcacc 219
      474 atg gcc cgc tcg ctg acc tgg cgc tgc tgc ccc tgg tgc ctg acg gag 267
      475 Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
      476  1               5                  10                  15
      477 gat gag aag gcc gcc gcc cgg gtg gac cag gag atc aac agg atc ctc 315
      478 Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
      479                 20                  25                  30
      480 ttg gag cag aag aag cag gac cgc ggg gag ctg aag ctg ctg ctt ttg 363
      481 Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu
      482             35                  40                  45
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      484 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
      485         50                  55                  60
      486 atc cac ggc gcc ggc tac tcg gag gag gag cgc aag ggc ttc cgg ccc 459
      487 Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
      488  65                  70                  75                  80
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      490 Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
      491                 85                  90                  95
      492 atg gag cgg ctg cag att cca ttc agc agg ccc gag agc aag cac cac 555
      493 Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
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Handwritten annotations:
1353 ← insert cumulative nucleotide total at right margin of each line.
see p. 22 for error explanation
29 ← insert
p.22
37 ← insert
insert <3097 and response
<400> 9 ← insert
see p.4
IMPORTANT

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496 Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
497       115              120              125
498 aag cgc tac gct gcg gcc atg cag tgg ctg tgg agg gat gcc ggc atc 651
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503 145              150              155              160
504 gtg tac tac ctg tcc cac ctg gag cgc atc acc gag gag ggc tac gtc 747
505 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
506              165              170              175
507 ccc aca gct cag gac gtg ctc cgc agc cgc atg ccc acc act ggc atc 795
508 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
509              180              185              190
510 aac gag tac tgc ttc tcc gtg cag aaa acc aac ctg cgg atc gtg gac 843
511 Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
512       195              200              205
513 gtc ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag 891
514 Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
515       210              215              220
516 aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag 939
517 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
518 225              230              235              240
519 tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca 987
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521              245              250              255
522 ttg ttt ggg act atc ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc 1035
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527       275              280              285
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530       290              295              300
531 gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac 1179
532 Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
533 305              310              315              320
534 acc ggg tgc gtg gac ggc ccc gag ggc agc aag aag ggc gca cga tcc 1227
535 Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Lys Lys Gly Ala Arg Ser
536              325              330              335
537 cga cgc ctt ttc agc cac tac aca tgt gcc aca gac aca cag aac atc 1275
538 Arg Arg Leu Phe Ser His Tyr Thr Cys Ala Thr Asp Thr Gln Asn Ile
539              340              345              350
540 cgc aag gtc ttc aag gac gtg cgg gac tcg gtg ctc gcc cgc tac ctg 1323
541 Arg Lys Val Phe Lys Asp Val Arg Asp Ser Val Leu Ala Arg Tyr Leu
542       355              360              365
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547 gcagggaccc tagtgtcctg gtctatctct ccagcctcgg cccacacgca agggagtcgg 1461
548 gggacggccc gctgctggcc gctctcttct ctgcctctca ccaggacagc cgccccccag 1521
549 ggtactcctg cccttgcttg actcagtttc cctcctttga aagggaagga gcaaaacggc 1581
550 catttgggat gccagggtgg atgaaaaggt gaagaaatca ggggattgag acttgggtgg 1641
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552 ccctctgtgg gtgacgcaca ccctgggatg gggctagtag agccttcagg cgccttcggg 1761
553 cgtggactct ggcgcactct agtggacagg agaaggaacg ccttccagga acctgtggac 1821
554 tagggggtgca gggacttccc tttgcaaggg gtaacagacc gctggaaaac actgtcactt 1881
555 tcagagctcg gtggctcaca gcgtgtcctg ccccggtttg cggacgagag aaatcgcggc 1941
556 ccacaagcat ccccccatccc ttgcaggctg ggggctgggc atgctgcatc ttaacctttt 2001
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562 <213> ORGANISM: Homosapiens
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567 <300> PUBLICATION INFORMATION: 10
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573 Arg Arg Ile Asp Arg His Leu Arg Ser Glu Ser Gln Arg Gln Arg Arg
574             20                  25                 30
575 gaa atc aag ctg ctc ctg ctg ggc acc agc aac tca ggc aag agc acc 156
576 Glu Ile Lys Leu Leu Leu Leu Gly Thr Ser Asn Ser Gly Lys Ser Thr
577          35                  40                 45
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579 Ile Val Lys Gln Met Lys Ile Ile His Ser Gly Gly Phe Asn Leu Glu
580       50                  55                 60
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583 65                  70                 75                 80
584 ctg acc cgc atc atc cgg gcc ctg gcc gcc ctc agg atc gac ttc cac 300
585 Leu Thr Arg Ile Ile Arg Ala Leu Ala Ala Leu Arg Ile Asp Phe His
586                 85                  90                 95
587 aac ccc gac cgc gcc tac gac gct gtg cag ctc ttt gcg ctg acg ggc 348
588 Asn Pro Asp Arg Ala Tyr Asp Ala Val Gln Leu Phe Ala Leu Thr Gly
589             100                 105                110
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591 Pro Ala Glu Ser Lys Gly Glu Ile Thr Pro Glu Leu Leu Gly Val Met
592             115                 120                125
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W- ... C

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598 145                   150                   155                   160
599 gag cgc atc gcc gca gct gac tat atc ccc act gtc gag gac atc ctg 540
600 Glu Arg Ile Ala Ala Ala Asp Tyr Ile Pro Thr Val Glu Asp Ile Leu
601                   165                   170                   175
602 cgc tcc cgg gac atg acc acg ggc att gtg gag aac aag ttc acc ttc 588
603 Arg Ser Arg Asp Met Thr Thr Gly Ile Val Glu Asn Lys Phe Thr Phe
604                   180                   185                   190
605 aag gag ctc acc ttc aag atg gtg gac gtg ggg ggg cag agg tca gag 636
606 Lys Glu Leu Thr Phe Lys Met Val Asp Val Gly Gly Gln Arg Ser Glu
607           195                   200                   205
608 cgc aaa aag tgg atc cac tgc ttc gag ggc gtc aca gcc atc atc ttc 684
609 Arg Lys Lys Trp Ile His Cys Phe Glu Gly Val Thr Ala Ile Ile Phe
610      210                   215                   220
611 tgt gtg gag ctc agc ggc tac gac ctg aaa ctc tac gag gat aac cag 732
612 Cys Val Glu Leu Ser Gly Tyr Asp Leu Lys Leu Tyr Glu Asp Asn Gln
613 225                   230                   235                   240
614 aca agt cgg atg gca gag agc ttg cgc ctc ttt gac tcc atc tgc aac 780
615 Thr Ser Arg Met Ala Glu Ser Leu Arg Leu Phe Asp Ser Ile Cys Asn
616                   245                   250                   255
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619                   260                   265                   270
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622      275                   280                   285
623 ccc gag tac aag ggc cag aac acg tac gag gag gcc gct gtc tac atc 924
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626 cag cgg cag ttt gaa gac ctg aac cgc aac aag gag acc aag gag atc 972
627 Gln Arg Gln Phe Glu Asp Leu Asn Arg Asn Lys Glu Thr Lys Glu Ile
628 305                   310                   315                   320
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631                   325                   330                   335
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633 Phe Asp Ala Val Thr Asp Val Ile Ile Gln Asn Asn Leu Lys Tyr Ile
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640 gcgtgctaga gaggcccaat ccaggggcag aaaacagggg gcctaaagaa tgtcccccac 1197
641 cccttggcct ctgcctcctt ggccccacat ttctgcaaac ataaatattt acggatagat 1257
642 tgctaggtag atagacacac acacatgcac acacacat ctggagatgg caaaatcctc 1317
643 taaaatgtcg aggtctcttg aagacttgag aagctgtcac aaggtcacta caagcccaac 1377
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RAW SEQUENCE LISTING   DATE: 07/06/2004
PATENT APPLICATION: US/10/663,650   TIME: 15:31:23

          Input Set : A:\US-972-Sequence.txt
          Output Set: N:\CRF4\07062004\J663650.raw

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   653 atttcaaatg cagttgagta ttctttttta aatgcagatt ttcaaaacat attttttttc 1977
   654 aggtggtctt ttttgtgtct ggcttgctga gtgtaaaagt tgttatctgg acgatctgtc 2037
   655 tctctgctcc aaagaaattt tggagtgagt ggcagtcctg cgccagcctc gcgggacacg 2097
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   662 ccaagggccg tgtgtaaata cgaactgcgc catggagagg agaggcactg ccggagccct 2517
   663 tgccagatct ccctccctct ctctgtgcag tagctgtgtg tccgaggtca gtgtgcggaa 2577
   664 tcacagccaa ggacgtgaag agatgtacgg gggaaagaga agctggggat tggatgaaag 2637
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2679 ←insert

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   668 <211> LENGTH: 29
   669 <212> TYPE: DNA
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see p.22
```
W--> 672 <220> FEATURE:
W--> 672 <223> OTHER INFORMATION:
W--> 672 <400> 11
```
29 ←insert
```
E--> 673 cgcaagcttg actgaggcca ccgcaccat
```
```
   675 <210> SEQ ID NO: 12
   676 <211> LENGTH: 29
   677 <212> TYPE: DNA
   678 <213> ORGANISM: Artificial Sequence
```
p.22
```
W--> 680 <220> FEATURE:
W--> 680 <223> OTHER INFORMATION:
W--> 680 <400> 12
```
29 ←insert
```
E--> 681 ctccttgttt cggttgctgc cctcggggc
```
```
   683 <210> SEQ ID NO: 13
   684 <211> LENGTH: 30
   685 <212> TYPE: DNA
   686 <213> ORGANISM: Artificial Sequence
```
p.22
```
W--> 688 <220> FEATURE:
W--> 688 <223> OTHER INFORMATION:
W--> 688 <400> 13
```
30 ←insert
```
E--> 689 ggccccgagg gcagcaaccg aaacaaggag
```
```
   691 <210> SEQ ID NO: 14
   692 <211> LENGTH: 37
   693 <212> TYPE: DNA
   694 <213> ORGANISM: Artificial Sequence
```
p.8

RAW SEQUENCE LISTING   DATE: 07/06/2004
PATENT APPLICATION: US/10/663,650   TIME: 15:31:23

Input Set : A:\US-972-Sequence.txt
Output Set: N:\CRF4\07062004\J663650.raw

```
W--> 696 <220> FEATURE:                        P.22
W--> 696 <223> OTHER INFORMATION:
W--> 696 <400> 14                                    37 <-- insert
E--> 697 gcattacgat gcggccgcag ctcctcagca aaggcca
     699 <210> SEQ ID NO: 15
     700 <211> LENGTH: 1122
     701 <212> TYPE: DNA
     702 <213> ORGANISM: Artificial Sequence
     704 <300> PUBLICATION INFORMATION:
     705 <301> AUTHORs: SEJAL M. MODY, MAURICE K. C. HO, SUSHMA A. JOSHI, and YUNG H. WONG
     706 <302> TITLE: Incorporation of GalphaZ-Specific Sequence at the Carboxyl Terminus
Increases the Promiscuity of Galpha16 toward Gi-Coupled Receptors
     707 <303> JOURNAL: The American Society for Pharmacology and Experimental Therapeutics
     708 <304> VOLUME: 57
     709 <306> PAGES: 13-23
     710 <307> DATE: 2000
W--> 711 <220> FEATURE:                        P.22
W--> 711 <223> OTHER INFORMATION:
W--> 711 <400> SEQUENCE: 15
     712 atg gcc cgc tcg ctg acc tgg cgc tgc tgc ccc tgg tgc ctg acg gag 48
     713 Met Ala Arg Ser Leu Thr Trp Arg Cys Cys Pro Trp Cys Leu Thr Glu
     714  1               5                   10                  15
     715 gat gag aag gcc gcc gcc cgg gtg gac cag gag atc aac agg atc ctc 96      see p.9
     716 Asp Glu Lys Ala Ala Ala Arg Val Asp Gln Glu Ile Asn Arg Ile Leu
     717             20                  25                  30
     718 ttg gag cag aag aag cag gac cgc ggg gag ctg aag ctg ctg ctt ttg 144
     719 Leu Glu Gln Lys Lys Gln Asp Arg Gly Glu Leu Lys Leu Leu Leu Leu
     720         35                  40                  45
     721 ggc cca ggc gag agc ggg aag agc acc ttc atc aag cag atg cgg atc 192
     722 Gly Pro Gly Glu Ser Gly Lys Ser Thr Phe Ile Lys Gln Met Arg Ile
     723     50                  55                  60
     724 atc cac ggc gcc ggc tac tcg gag gag gag cgc aag ggc ttc cgg ccc 240
     725 Ile His Gly Ala Gly Tyr Ser Glu Glu Glu Arg Lys Gly Phe Arg Pro
     726 65                  70                  75                  80
     727 ctg gtc tac cag aac atc ttc gtg tcc atg cgg gcc atg atc gag gcc 288
     728 Leu Val Tyr Gln Asn Ile Phe Val Ser Met Arg Ala Met Ile Glu Ala
     729                 85                  90                  95
     730 atg gag cgg ctg cag att cca ttc agc agg ccc gag agc aag cac cac 336
     731 Met Glu Arg Leu Gln Ile Pro Phe Ser Arg Pro Glu Ser Lys His His
     732             100                 105                 110
     733 gct agc ctg gtc atg agc cag gac ccc tat aaa gtg acc acg ttt gag 384
     734 Ala Ser Leu Val Met Ser Gln Asp Pro Tyr Lys Val Thr Thr Phe Glu
     735         115                 120                 125
     736 aag cgc tac gct gcg gcc atg cag tgg ctg tgg agg gat gcc ggc atc 432
     737 Lys Arg Tyr Ala Ala Ala Met Gln Trp Leu Trp Arg Asp Ala Gly Ile
     738     130                 135                 140
     739 cgg gcc tgc tat gag cgt cgg cgg gaa ttc cac ctg ctc gat tca gcc 480
     740 Arg Ala Cys Tyr Glu Arg Arg Arg Glu Phe His Leu Leu Asp Ser Ala
     741 145                 150                 155                 160
     742 gtg tac tac ctg tcc cac ctg gag cgc atc acc gag gag ggc tac gtc 528
```

Input Set : A:\US-972-Sequence.txt
Output Set: N:\CRF4\07062004\J663650.raw

```
743 Val Tyr Tyr Leu Ser His Leu Glu Arg Ile Thr Glu Glu Gly Tyr Val
744               165              170              175
745 ccc aca gct cag gac gtg ctc cgc agc cgc atg ccc acc act ggc atc 576
746 Pro Thr Ala Gln Asp Val Leu Arg Ser Arg Met Pro Thr Thr Gly Ile
747           180              185              190
748 aac gag tac tgc ttc tcc gtg cag aaa acc aac ctg cgg atc gtg gac 624
749 Asn Glu Tyr Cys Phe Ser Val Gln Lys Thr Asn Leu Arg Ile Val Asp
750           195              200              205
751 gtc ggg ggc cag aag tca gag cgt aag aaa tgg atc cat tgt ttc gag 672
752 Val Gly Gly Gln Lys Ser Glu Arg Lys Lys Trp Ile His Cys Phe Glu
753           210              215              220
754 aac gtg atc gcc ctc atc tac ctg gcc tca ctg agt gaa tac gac cag 720
755 Asn Val Ile Ala Leu Ile Tyr Leu Ala Ser Leu Ser Glu Tyr Asp Gln
756 225              230              235              240
757 tgc ctg gag gag aac aac cag gag aac cgc atg aag gag agc ctc gca 768
758 Cys Leu Glu Glu Asn Asn Gln Glu Asn Arg Met Lys Glu Ser Leu Ala
759           245              250              255
760 ttg ttt ggg act atc ctg gaa cta ccc tgg ttc aaa agc aca tcc gtc 816
761 Leu Phe Gly Thr Ile Leu Glu Leu Pro Trp Phe Lys Ser Thr Ser Val
762           260              265              270
763 atc ctc ttt ctc aac aaa acc gac atc ctg gag gag aaa atc ccc acc 864
764 Ile Leu Phe Leu Asn Lys Thr Asp Ile Leu Glu Glu Lys Ile Pro Thr
765           275              280              285
766 tcc cac ctg gct acc tat ttc ccc agt ttc cag ggc cct aag cag gat 912
767 Ser His Leu Ala Thr Tyr Phe Pro Ser Phe Gln Gly Pro Lys Gln Asp
768     290              295              300
769 gct gag gca gcc aag agg ttc atc ctg gac atg tac acg agg atg tac 960
770 Ala Glu Ala Ala Lys Arg Phe Ile Leu Asp Met Tyr Thr Arg Met Tyr
771 305              310              315              320
772 acc ggg tgc gtg gac ggc ccc gag ggc agc aac cgc aac aag gag acc 1008
773 Thr Gly Cys Val Asp Gly Pro Glu Gly Ser Asn Arg Asn Lys Glu Thr
774           325              330              335
775 aag gag atc tac tcc cac ttc acc tgc gcc acc gac acc agt aac atc 1056
776 Lys Glu Ile Tyr Ser His Phe Thr Cys Ala Thr Asp Thr Ser Asn Ile
777           340              345              350
778 cag ttt gtc ttc gac gcg gtg aca gac gtc atc ata cag aac aat ctc 1104
779 Gln Phe Val Phe Asp Ala Val Thr Asp Val Ile Ile Gln Asn Asn Leu
780     355              360              365
E--> 781 aag tac att ggc ctt tgc
782 Lys Tyr Ile Gly Leu Cys
783     370
785 <210> SEQ ID NO: 16
786 <211> LENGTH: 2529
787 <212> TYPE: DNA
788 <213> ORGANISM: Mus musculus
790 <300> PUBLICATION INFORMATION:
791 <308> DATABASE ACCESSION NO: GENBANK AY032622
793 <300> PUBLICATION INFORMATION: 16
794 atg ctt ttc tgg gca gct cac ctg ctg ctc agc ctg cag ctg gcc gtt 48
```

1122 ← insert

insert <3097 and response

p.13

```
795 Met Leu Phe Trp Ala Ala His Leu Leu Leu Ser Leu Gln Leu Ala Val
796  1               5                   10                  15
797 gct tac tgc tgg gct ttc agc tgc caa agg aca gaa tcc tct cca ggt 96
798 Ala Tyr Cys Trp Ala Phe Ser Cys Gln Arg Thr Glu Ser Ser Pro Gly
799             20                  25                  30
800 ttc agc ctc cct ggg gac ttc ctc ctg gca ggc ctg ttc tcc ctc cat 144
801 Phe Ser Leu Pro Gly Asp Phe Leu Leu Ala Gly Leu Phe Ser Leu His
802         35                  40                  45
803 gct gac tgt ctg cag gtg aga cac aga cct ctg gtg aca agt tgt gac 192
804 Ala Asp Cys Leu Gln Val Arg His Arg Pro Leu Val Thr Ser Cys Asp
805     50                  55                  60
806 agg tct gac agc ttc aac ggc cat ggc tat cac ctc ttc caa gcc atg 240
807 Arg Ser Asp Ser Phe Asn Gly His Gly Tyr His Leu Phe Gln Ala Met
808 65                  70                  75                  80
809 cgg ttc acc gtt gag gag ata aac aac tcc aca gct ctg ctt ccc aac 288
810 Arg Phe Thr Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn
811                 85                  90                  95
812 atc acc ctg ggg tat gaa ctg tat gac gtg tgc tca gag tct tcc aat 336
813 Ile Thr Leu Gly Tyr Glu Leu Tyr Asp Val Cys Ser Glu Ser Ser Asn
814                 100                 105                 110
815 gtc tat gcc acc ctg agg gtg ccc gcc cag caa ggg aca ggc cac cta 384
816 Val Tyr Ala Thr Leu Arg Val Pro Ala Gln Gln Gly Thr Gly His Leu
817             115                 120                 125
818 gag atg cag aga gat ctt cgc aac cac tcc tcc aag gtg gtg gca ctc 432
819 Glu Met Gln Arg Asp Leu Arg Asn His Ser Ser Lys Val Val Ala Leu
820     130                 135                 140
821 att ggg cct gat aac act gac cac gct gtc acc act gct gcc ctg ctg 480
822 Ile Gly Pro Asp Asn Thr Asp His Ala Val Thr Thr Ala Ala Leu Leu
823 145                 150                 155                 160
824 agc cct ttt ctg atg ccc ctg gtc agc tat gag gcg agc agc gtg atc 528
825 Ser Pro Phe Leu Met Pro Leu Val Ser Tyr Glu Ala Ser Ser Val Ile
826                 165                 170                 175
827 ctc agt ggg aag cgc aag ttc ccg tcc ttc ttg cgc acc atc ccc agc 576
828 Leu Ser Gly Lys Arg Lys Phe Pro Ser Phe Leu Arg Thr Ile Pro Ser
829             180                 185                 190
830 gat aag tac cag gtg gaa gtc ata gtg cgg ctg ctg cag agc ttc ggc 624
831 Asp Lys Tyr Gln Val Glu Val Ile Val Arg Leu Leu Gln Ser Phe Gly
832             195                 200                 205
833 tgg gtc tgg atc tcg ctc gtt ggc agc tat ggt gac tac ggg cag ctg 672
834 Trp Val Trp Ile Ser Leu Val Gly Ser Tyr Gly Asp Tyr Gly Gln Leu
835     210                 215                 220
836 ggc gta cag gcg ctg gag gag ctg gcc act cca cgg ggc atc tgc gtc 720
837 Gly Val Gln Ala Leu Glu Glu Leu Ala Thr Pro Arg Gly Ile Cys Val
838 225                 230                 235                 240
839 gcc ttc aag gac gtg gtg cct ctc tcc gcc cag gcg ggt gac cca agg 768
840 Ala Phe Lys Asp Val Val Pro Leu Ser Ala Gln Ala Gly Asp Pro Arg
841             245                 250                 255
842 atg cag cgc atg atg ctg cgt ctg gct cga gcc agg acc acc gtg gtc 816
843 Met Gln Arg Met Met Leu Arg Leu Ala Arg Ala Arg Thr Thr Val Val
```

```
844              260                265                270
845 gtg gtc ttc tct aac cgg cac ctg gct gga gtg ttc ttc agg tct gtg 864
846 Val Val Phe Ser Asn Arg His Leu Ala Gly Val Phe Phe Arg Ser Val
847         275          .         280                285
848 gtg ctg gcc aac ctg act ggc aaa gtg tgg atc gcc tcc gaa gac tgg 912
849 Val Leu Ala Asn Leu Thr Gly Lys Val Trp Ile Ala Ser Glu Asp Trp
850      290                295                300
851 gcc atc tcc acg tac atc acc aat gtg ccc ggg atc cag ggc att ggg 960
852 Ala Ile Ser Thr Tyr Ile Thr Asn Val Pro Gly Ile Gln Gly Ile Gly
853 305                310                315                320
854 acg gtg ctg ggg gtg gcc atc cag cag aga caa gtc cct ggc ctg aag 1008
855 Thr Val Leu Gly Val Ala Ile Gln Gln Arg Gln Val Pro Gly Leu Lys
856              325                330                335
857 gag ttt gaa gag tcc tat gtc cag gca gtg atg ggt gct ccc aga act 1056
858 Glu Phe Glu Glu Ser Tyr Val Gln Ala Val Met Gly Ala Pro Arg Thr
859              340                345   .            350
860 tgc cca gag ggg tcc tgg tgc ggc act aac cag ctg tgc agg gag tgt 1104
861 Cys Pro Glu Gly Ser Trp Cys Gly Thr Asn Gln Leu Cys Arg Glu Cys
862         355                360                365
863 cac gct ttc acg aca tgg aac atg ccc gag ctt gga gcc ttc tcc atg 1152
864 His Ala Phe Thr Thr Trp Asn Met Pro Glu Leu Gly Ala Phe Ser Met
865      370                375                380
866 agc gct gcc tac aat gtg tat gag gct gtg tat gct gtg gcc cac ggc 1200
867 Ser Ala Ala Tyr Asn Val Tyr Glu Ala Val Tyr Ala Val Ala His Gly
868 385                390                395                400
869 ctc cac cag ctc ctg gga tgt acc tct ggg acc tgt gcc aga ggc cca 1248
870 Leu His Gln Leu Leu Gly Cys Thr Ser Gly Thr Cys Ala Arg Gly Pro
871              405                410                415
872 gtc tac ccc tgg cag ctt ctt cag cag atc tac aag gtg aat ttc ctt 1296
873 Val Tyr Pro Trp Gln Leu Leu Gln Gln Ile Tyr Lys Val Asn Phe Leu
874              420                425                430
875 cta cat aag aag act gta gca ttc gat gac aag ggg gac cct cta ggt 1344
876 Leu His Lys Lys Thr Val Ala Phe Asp Asp Lys Gly Asp Pro Leu Gly
877 .        435                440                445
878 tat tat gac atc atc gcc tgg gac tgg aat gga cct gaa tgg acc ttt 1392
879 Tyr Tyr Asp Ile Ile Ala Trp Asp Trp Asn Gly Pro Glu Trp Thr Phe
880      450                455                460
881 gag gtc att ggt tct gcc tca ctg tct cca gtt cat cta gac ata aat 1440
882 Glu Val Ile Gly Ser Ala Ser Leu Ser Pro Val His Leu Asp Ile Asn
883 465                470                475                480
884 aag aca aaa atc cag tgg cac ggg aag aac aat cag gtg cct gtg tca 1488
885 Lys Thr Lys Ile Gln Trp His Gly Lys Asn Asn Gln Val Pro Val Ser
886              485                490                495
887 gtg tgt acc agg gac tgt ctc gaa ggg cac cac agg ttg gtc atg ggt 1536
888 Val Cys Thr Arg Asp Cys Leu Glu Gly His His Arg Leu Val Met Gly
889         500                505                510
890 tcc cac cac tgc tgc ttc gag tgc atg ccc tgt gaa gct ggg aca ttt 1584
891 Ser His His Cys Cys Phe Glu Cys Met Pro Cys Glu Ala Gly Thr Phe
892         515                520                525
```

```
893 ctc aac acg agt gag ctt cac acc tgc cag cct tgt gga aca gaa gaa 1632
894 Leu Asn Thr Ser Glu Leu His Thr Cys Gln Pro Cys Gly Thr Glu Glu
895      530                   535                   540
896 tgg gcc cct gag ggg agc tca gcc tgc ttc tca cgc acc gtg gag ttc 1680
897 Trp Ala Pro Glu Gly Ser Ser Ala Cys Phe Ser Arg Thr Val Glu Phe
898 545                   550                   555                   560
899 ttg ggg tgg cat gaa ccc atc tct ttg gtg cta tta gca gct aac acg 1728
900 Leu Gly Trp His Glu Pro Ile Ser Leu Val Leu Leu Ala Ala Asn Thr
901                   565                   570                   575
902 cta ttg ctg ctg ctg ctg att ggg act gct ggc ctg ttt gcc tgg cgt 1776
903 Leu Leu Leu Leu Leu Leu Ile Gly Thr Ala Gly Leu Phe Ala Trp Arg
904              580                   585                   590
905 ctt cac acg cct gtt gtg agg tca gct ggg ggt agg ctg tgc ttc ctc 1824
906 Leu His Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu
907           595                   600                   605
908 atg ctg ggt tcc ttg gta gct ggg agt tgc agc ctc tac agc ttc ttc 1872
909 Met Leu Gly Ser Leu Val Ala Gly Ser Cys Ser Leu Tyr Ser Phe Phe
910      610                   615                   620
911 ggg aag ccc acg gtg ccc gcg tgc ttg ctg cgt cag ccc ctc ttt tct 1920
912 Gly Lys Pro Thr Val Pro Ala Cys Leu Leu Arg Gln Pro Leu Phe Ser
913 625                   630                   635                   640
914 ctc ggg ttt gcc att ttc ctc tcc tgt ctg aca atc cgc tcc ttc caa 1968
915 Leu Gly Phe Ala Ile Phe Leu Ser Cys Leu Thr Ile Arg Ser Phe Gln
916                   645                   650                   655
917 ctg gtc atc atc ttc aag ttt tct acc aag gta ccc aca ttc tac cac 2016
918 Leu Val Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His
919                   660                   665                   670
920 act tgg gcc caa aac cat ggt gcc gga ata ttc gtc att gtc agc tcc 2064
921 Thr Trp Ala Gln Asn His Gly Ala Gly Ile Phe Val Ile Val Ser Ser
922              675                   680                   685
923 acg gtc cat ttg ttc ctc tgt ctc acg tgg ctt gca atg tgg acc cca 2112
924 Thr Val His Leu Phe Leu Cys Leu Thr Trp Leu Ala Met Trp Thr Pro
925      690                   695                   700
926 cgg ccc acc agg gag tac cag cgc ttc ccc cat ctg gtg att ctt gag 2160
927 Arg Pro Thr Arg Glu Tyr Gln Arg Phe Pro His Leu Val Ile Leu Glu
928 705                   710                   715                   720
929 tgc aca gag gtc aac tct gtg ggc ttc ctg gtg gct ttc gca cac aac 2208
930 Cys Thr Glu Val Asn Ser Val Gly Phe Leu Val Ala Phe Ala His Asn
931                   725                   730                   735
932 atc ctc ctc tcc atc agc acc ttt gtc tgc agc tac ctg ggt aag gaa 2256
933 Ile Leu Leu Ser Ile Ser Thr Phe Val Cys Ser Tyr Leu Gly Lys Glu
934              740                   745                   750
935 ctg ccg gag aac tat aac gaa gcc aaa tgt gtc acc ttc agc ctg ctc 2304
936 Leu Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu
937           755                   760                   765
938 ctc cac ttc gta tcc tgg atc gct ttc ttc acc atg tcc agc att tac 2352
939 Leu His Phe Val Ser Trp Ile Ala Phe Phe Thr Met Ser Ser Ile Tyr
940      770                   775                   780
941 cag ggc agc tac cta ccc gcg gtc aat gtg ctg gca ggg ctg gcc act 2400
```

```
   942 Gln Gly Ser Tyr Leu Pro Ala Val Asn Val Leu Ala Gly Leu Ala Thr
   943 785                 790             795                 800
   944 ctg agt ggc ggc ttc agc ggc tat ttc ctc cct aaa tgc tac gtg att 2448
   945 Leu Ser Gly Gly Phe Ser Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile
   946                 805                 810                 815
   947 ctc tgc cgt cca gaa ctc aac aac aca gaa cac ttt cag gcc tcc atc 2496
   948 Leu Cys Arg Pro Glu Leu Asn Asn Thr Glu His Phe Gln Ala Ser Ile
   949                 820                 825                 830
E-->950 cag gac tac acg agg cgc tgc ggc act acc tga
   951 Gln Asp Tyr Thr Arg Arg Cys Gly Thr Thr
   952             835                 840
   954 <210> SEQ ID NO: 17
   955 <211> LENGTH: 2532
   956 <212> TYPE: DNA
   957 <213> ORGANISM: Mus musculus
   959 <300> PUBLICATION INFORMATION:
   960 <308> DATABASE ACCESSION NO: GENBANK AY032623
   962 <300> PUBLICATION INFORMATION: 17
   963 atg gga ccc cag gcg agg aca ctc cat ttg ctg ttt ctc ctg ctg cat 48
   964 Met Gly Pro Gln Ala Arg Thr Leu His Leu Leu Phe Leu Leu Leu His
   965  1               5                   10                  15
   966 gct ctg cct aag cca gtc atg ctg gta ggg aac tcc gac ttt cac ctg 96
   967 Ala Leu Pro Lys Pro Val Met Leu Val Gly Asn Ser Asp Phe His Leu
   968                 20                  25                  30
   969 gct ggg gac tac ctc ctg ggt ggc ctc ttt acc ctc cat gcc aac gtg 144
   970 Ala Gly Asp Tyr Leu Leu Gly Gly Leu Phe Thr Leu His Ala Asn Val
   971             35                  40                  45
   972 aag agt gtc tct cac ctc agc tac ctg cag gtg ccc aag tgc aat gag 192
   973 Lys Ser Val Ser His Leu Ser Tyr Leu Gln Val Pro Lys Cys Asn Glu
   974         50                  55                  60
   975 tac aac atg aag gtg ttg ggc tac aac ctc atg cag gcc atg cga ttc 240
   976 Tyr Asn Met Lys Val Leu Gly Tyr Asn Leu Met Gln Ala Met Arg Phe
   977  65                  70                  75                  80
   978 gcc gtg gag gaa atc aac aac tgt agc tct ttg ctg ccc ggc gtg ctg 288
   979 Ala Val Glu Glu Ile Asn Asn Cys Ser Ser Leu Leu Pro Gly Val Leu
   980                 85                  90                  95
   981 ctc ggc tac gag atg gtg gat gtc tgc tac ctc tcc aac aat atc cag 336
   982 Leu Gly Tyr Glu Met Val Asp Val Cys Tyr Leu Ser Asn Asn Ile Gln
   983             100                 105                 110
   984 cct ggg ctc tac ttc ctg tca cag ata gat gac ttc ctg ccc atc ctc 384
   985 Pro Gly Leu Tyr Phe Leu Ser Gln Ile Asp Asp Phe Leu Pro Ile Leu
   986         115                 120                 125
   987 aaa gac tac agc cag tac agg ccc caa gtg gtg gct gtt att ggc cca 432
   988 Lys Asp Tyr Ser Gln Tyr Arg Pro Gln Val Val Ala Val Ile Gly Pro
   989     130                 135                 140
   990 gac aac tct gag tct gcc atc acc gtg tcc aac att ctc tcc tac ttc 480
   991 Asp Asn Ser Glu Ser Ala Ile Thr Val Ser Asn Ile Leu Ser Tyr Phe
   992 145                 150                 155                 160
   993 ctc gtg cca cag gtc aca tat agc gcc atc acc gac aag ctg caa gac 528
```

RAW SEQUENCE LISTING   DATE: 07/06/2004
PATENT APPLICATION: US/10/663,650   TIME: 15:31:23

Input Set : A:\US-972-Sequence.txt
Output Set: N:\CRF4\07062004\J663650.raw

```
994  Leu Val Pro Gln Val Thr Tyr Ser Ala Ile Thr Asp Lys Leu Gln Asp
995              165             170             175
996  aag cgg cgc ttc cct gcc atg ctg cgc act gtg ccc agc gcc acc cac 576
997  Lys Arg Arg Phe Pro Ala Met Leu Arg Thr Val Pro Ser Ala Thr His
998              180             185             190
999  cac atc gag gcc atg gtg caa ctg atg gtt cac ttc cag tgg aac tgg 624
1000 His Ile Glu Ala Met Val Gln Leu Met Val His Phe Gln Trp Asn Trp
1001             195             200             205  .
1002 atc gtg gtg ctg gtg agc gat gac gat tat ggc cga gag aac agc cac 672
1003 Ile Val Val Leu Val Ser Asp Asp Asp Tyr Gly Arg Glu Asn Ser His
1004        210             215             220
1005 ctg ctg agc cag cgt ctg acc aac act ggc gac atc tgc att gcc ttc 720
1006 Leu Leu Ser Gln Arg Leu Thr Asn Thr Gly Asp Ile Cys Ile Ala Phe
1007 225             230             235             240
1008 cag gag gtt ctg ccc gta cca gaa ccc aac cag gct gtg agg cct gag 768.
1009 Gln Glu Val Leu Pro Val Pro Glu Pro Asn Gln Ala Val Arg Pro Glu
1010             245             250  .          255
1011 gag cag gac caa ctg gac aac atc ctg gac aag ctg cgg cgg act tcg 816
1012 Glu Gln Asp Gln Leu Asp Asn Ile Leu Asp Lys Leu Arg Arg Thr Ser
1013             260             265             270
1014 gcg cgt gtg gtg gtg ata ttc tcg ccg gag ctg agc ctg cac aac ttc 864
1015 Ala Arg Val Val Val Ile Phe Ser Pro Glu Leu Ser Leu His Asn Phe
1016             275             280             285
1017 ttc cgt gag gtg ctg cgc tgg aac ttc acg ggc ttt gtg tgg att gcc 912
1018 Phe Arg Glu Val Leu Arg Trp Asn Phe Thr Gly Phe Val Trp Ile Ala
1019        290  .          295             300
1020 tct gag tcc tgg gcc atc gac cct gtt cta cac aac ctc aca gag ctg 960
1021 Ser Glu Ser Trp Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu
1022 305     .           310             315             320
1023 cgc cac acg ggc act ttc ctg ggt gtc acc atc cag agg gtg tcc atc 1008
1024 Arg His Thr Gly Thr Phe Leu Gly Val Thr Ile Gln Arg Val Ser Ile
1025             325     .           330     .           335
1026 cct ggc ttc agc cag ttc cga gtg cgc cat gac aag cca ggg tat cgc 1056
1027 Pro Gly Phe Ser Gln Phe Arg Val Arg His Asp Lys Pro Gly Tyr Arg
1028             340             345             350
1029 atg cct aac gag acc agc ctg cgg act acc tgt aac cag gac tgc gac 1104
1030 Met Pro Asn Glu Thr Ser Leu Arg Thr Thr Cys Asn Gln Asp Cys Asp
1031             355             360             365
1032 gcc tgc atg aac atc act gag tcc ttc aac aac gtt ctc atg ctt tcg 1152
1033 Ala Cys Met Asn Ile Thr Glu Ser Phe Asn Asn Val Leu Met Leu Ser
1034        370             375             380
1035 ggg gag cgt gtg gtc tac agc gtg tac tcg gcc gtc tac gcg gtg gcc 1200
1036 Gly Glu Arg Val Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala
1037 385             390             395             400
1038 cac acc ctc cac aga ctc ctc cac tgc aat cag gtc cgc tgc acc aag 1248
1039 His Thr Leu His Arg Leu Leu His Cys Asn Gln Val Arg Cys Thr Lys
1040             405             410             415
1041 caa atc gtc tat cca tgg cag cta ctc agg gag atc tgg cat gtc aac 1296
1042 Gln Ile Val Tyr Pro Trp Gln Leu Leu Arg Glu Ile Trp His Val Asn
```

```
1043              420                 425                 430
1044 ttc acg ctc ctg ggc aac cag ctc ttc ttc gac gaa caa ggg gac atg 1344
1045 Phe Thr Leu Leu Gly Asn Gln Leu Phe Phe Asp Glu Gln Gly Asp Met
1046         435                 440                 445
1047 ccg atg ctc ctg gac atc atc cag tgg cag tgg ggc ctg agc cag aac 1392
1048 Pro Met Leu Leu Asp Ile Ile Gln Trp Gln Trp Gly Leu Ser Gln Asn
1049      450                 455                 460
1050 ccc ttc caa agc atc gcc tcc tac tcc ccc acc gag acg agg ctg acc 1440
1051 Pro Phe Gln Ser Ile Ala Ser Tyr Ser Pro Thr Glu Thr Arg Leu Thr
1052 465                 470                 475                 480
1053 tac att agc aat gtg tcc tgg tac acc ccc aac aac acg gtc ccc ata 1488
1054 Tyr Ile Ser Asn Val Ser Trp Tyr Thr Pro Asn Asn Thr Val Pro Ile
1055              485                 490                 495
1056 tcc atg tgt tct aag agt tgc cag cct ggg caa atg aaa aaa ccc ata 1536
1057 Ser Met Cys Ser Lys Ser Cys Gln Pro Gly Gln Met Lys Lys Pro Ile
1058              500                 505                 510
1059 ggc ctc cac cca tgc tgc ttc gag tgt gtg gac tgt ccg ccg gac acc 1584
1060 Gly Leu His Pro Cys Cys Phe Glu Cys Val Asp Cys Pro Pro Asp Thr
1061         515                 520                 525
1062 tac ctc aac cga tca gta gat gag ttt aac tgt ctg tcc tgc ccg ggt 1632
1063 Tyr Leu Asn Arg Ser Val Asp Glu Phe Asn Cys Leu Ser Cys Pro Gly
1064      530                 535                 540
1065 tcc atg tgg tct tac aag aac aac atc gct tgc ttc aag cgg cgg ctg 1680
1066 Ser Met Trp Ser Tyr Lys Asn Asn Ile Ala Cys Phe Lys Arg Arg Leu
1067 545                 550                 555                 560
1068 gcc ttc ctg gag tgg cac gaa gtg ccc act atc gtg gtg acc atc ctg 1728
1069 Ala Phe Leu Glu Trp His Glu Val Pro Thr Ile Val Val Thr Ile Leu
1070              565                 570                 575
1071 gcc gcc ctg ggc ttc atc agt acg ctg gcc att ctg ctc atc ttc tgg 1776
1072 Ala Ala Leu Gly Phe Ile Ser Thr Leu Ala Ile Leu Leu Ile Phe Trp
1073         580                 585                 590
1074 aga cat ttc cag acg ccc atg gtg cgc tcg gcg ggc ggc ccc atg tgc 1824
1075 Arg His Phe Gln Thr Pro Met Val Arg Ser Ala Gly Gly Pro Met Cys
1076         595                 600                 605
1077 ttc ctg atg ctg gtg ccc ctg ctg ctg gcg ttc ggg atg gtc ccc gtg 1872
1078 Phe Leu Met Leu Val Pro Leu Leu Leu Ala Phe Gly Met Val Pro Val
1079      610                 615                 620
1080 tat gtg ggc ccc ccc acg gtc ttc tcc tgt ttc tgc cgc cag gct ttc 1920
1081 Tyr Val Gly Pro Pro Thr Val Phe Ser Cys Phe Cys Arg Gln Ala Phe
1082 625                 630                 635                 640
1083 ttc acc gtt tgc ttc tcc gtc tgc ctc tcc tgc atc acg gtg cgc tcc 1968
1084 Phe Thr Val Cys Phe Ser Val Cys Leu Ser Cys Ile Thr Val Arg Ser
1085              645                 650                 655
1086 ttc cag att gtg tgc gtc ttc aag atg gcc aga cgc ctg cca agc gcc 2016
1087 Phe Gln Ile Val Cys Val Phe Lys Met Ala Arg Arg Leu Pro Ser Ala
1088         660                 665                 670
1089 tac ggt ttc tgg atg cgt tac cac ggg ccc tac gtc ttc gtg gcc ttc 2064
1090 Tyr Gly Phe Trp Met Arg Tyr His Gly Pro Tyr Val Phe Val Ala Phe
1091         675                 680                 685
```

```
1092 atc acg gcc gtc aag gtg gcc ctg gtg gcg ggc aac atg ctg gcc acc 2112
1093 Ile Thr Ala Val Lys Val Ala Leu Val Ala Gly Asn Met Leu Ala Thr
1094         690               695               700
1095 acc atc aac ccc att ggc cgg acc gac ccc gat gac ccc aat atc ata 2160
1096 Thr Ile Asn Pro Ile Gly Arg Thr Asp Pro Asp Asp Pro Asn Ile Ile
1097 705               710               715               720
1098 atc ctc tcc tgc cac cct aac tac cgc aac ggg cta ctc ttc aac acc 2208
1099 Ile Leu Ser Cys His Pro Asn Tyr Arg Asn Gly Leu Leu Phe Asn Thr
1100               725               730               735
1101 agc atg gac ttg ctg ctg tcc gtg ctg ggt ttc agc ttc gcg tac gtg 2256
1102 Ser Met Asp Leu Leu Leu Ser Val Leu Gly Phe Ser Phe Ala Tyr Val
1103               740               745               750
1104 ggc aag gaa ctg ccc acc aac tac aac gaa gcc aag ttc atc acc ctc 2304
1105 Gly Lys Glu Leu Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu
1106               755               760               765
1107 agc atg acc ttc tcc ttc acc tcc tcc atc tcc ctc tgc acg ttc atg 2352
1108 Ser Met Thr Phe Ser Phe Thr Ser Ser Ile Ser Leu Cys Thr Phe Met
1109         770               775               780
1110 tct gtc cac gat ggc gtg ctg gtc acc atc atg gat ctc ctg gtc act 2400
1111 Ser Val His Asp Gly Val Leu Val Thr Ile Met Asp Leu Leu Val Thr
1112 785               790               795               800
1113 gtg ctc aac ttt ctg gcc atc ggc ttg ggg tac ttt ggc ccc aaa tgt 2448
1114 Val Leu Asn Phe Leu Ala Ile Gly Leu Gly Tyr Phe Gly Pro Lys Cys
1115               805               810               815
1116 tac atg atc ctt ttc tac ccg gag cgc aac act tca gct tat ttc aat 2496
1117 Tyr Met Ile Leu Phe Tyr Pro Glu Arg Asn Thr Ser Ala Tyr Phe Asn
1118               820               825               830
```

E--> **1119 agc atg att cag ggc tac acg atg agg aag agc tag**
```
1120 Ser Met Ile Gln Gly Tyr Thr Met Arg Lys Ser
1121         835               840
```
2532←insert

```
1123 <210> SEQ ID NO: 18
1124 <211> LENGTH: 2577
1125 <212> TYPE: DNA
1126 <213> ORGANISM: Mus musculus
```

P.19

```
1128 <400> SEQUENCE: 18
1129 atg cca gct ttg gct atc atg ggt ctc agc ctg gct gct ttc ctg gag 48
1130 Met Pro Ala Leu Ala Ile Met Gly Leu Ser Leu Ala Ala Phe Leu Glu
1131 1               5                 10                15
1132 ctt ggg atg ggg gcc tct ttg tgt ctg tca cag caa ttc aag gca caa 96
1133 Leu Gly Met Gly Ala Ser Leu Cys Leu Ser Gln Gln Phe Lys Ala Gln
1134         20                25                30
1135 ggg gac tac ata ctg ggc ggg cta ttt ccc ctg ggc tca acc gag gag 144
1136 Gly Asp Tyr Ile Leu Gly Gly Leu Phe Pro Leu Gly Ser Thr Glu Glu
1137         35                40                45
1138 gcc act ctc aac cag aga aca caa ccc aac agc atc ccg tgc aac agg 192
1139 Ala Thr Leu Asn Gln Arg Thr Gln Pro Asn Ser Ile Pro Cys Asn Arg
1140         50                55                60
1141 ttc tca ccc ctt ggt ttg ttc ctg gcc atg gct atg aag atg gct gtg 240
1142 Phe Ser Pro Leu Gly Leu Phe Leu Ala Met Ala Met Lys Met Ala Val
```

```
1143  65                    70                   75                    80
1144 gag gag atc aac aat gga tct gcc ttg ctc cct ggg ctg cgg ctg ggc 288
1145 Glu Glu Ile Asn Asn Gly Ser Ala Leu Leu Pro Gly Leu Arg Leu Gly
1146                   85                    90                   95
1147 tat gac cta ttt gac aca tgc tcc gag cca gtg gtc acc atg aaa tcc 336
1148 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Thr Met Lys Ser
1149               100                   105                  110
1150 agt ctc atg ttc ctg gcc aag gtg ggc agt caa agc att gct gcc tac 384
1151 Ser Leu Met Phe Leu Ala Lys Val Gly Ser Gln Ser Ile Ala Ala Tyr
1152          115                   120                   125
1153 tgc aac tac aca cag tac caa ccc cgt gtg ctg gct gtc atc ggc ccc 432
1154 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
1155      130                   135                   140
1156 cac tca tca gag ctt gcc ctc att aca ggc aag ttc ttc agc ttc ttc 480
1157 His Ser Ser Glu Leu Ala Leu Ile Thr Gly Lys Phe Phe Ser Phe Phe
1158 145                   150                   155                   160
1159 ctc atg cca cag gtc agc tat agt gcc agc atg gat cgg cta agt gac 528
1160 Leu Met Pro Gln Val Ser Tyr Ser Ala Ser Met Asp Arg Leu Ser Asp
1161               165                   170                   175
1162 cgg gaa acg ttt cca tcc ttc ttc cgc aca gtg ccc agt gac cgg gtg 576
1163 Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
1164               180                   185                   190
1165 cag ctg cag gca gtt gtg act ctg ttg cag aac ttc agc tgg aac tgg 624
1166 Gln Leu Gln Ala Val Val Thr Leu Leu Gln Asn Phe Ser Trp Asn Trp
1167          195                   200                   205
1168 gtg gcc gcc tta ggg agt gat gat gac tat ggc cgg gaa ggt ctg agc 672
1169 Val Ala Ala Leu Gly Ser Asp Asp Asp Tyr Gly Arg Glu Gly Leu Ser
1170      210                   215                   220
1171 atc ttt tct agt ctg gcc aat gca cga ggt atc tgc atc gca cat gag 720
1172 Ile Phe Ser Ser Leu Ala Asn Ala Arg Gly Ile Cys Ile Ala His Glu
1173 225                   230                   235                   240
1174 ggc ctg gtg cca caa cat gac act agt ggc caa cag ttg ggc aag gtg 768
1175 Gly Leu Val Pro Gln His Asp Thr Ser Gly Gln Gln Leu Gly Lys Val
1176               245                   250                   255
1177 ctg gat gta cta cgc caa gtg aac caa agt aaa gta caa gtg gtg gtg 816
1178 Leu Asp Val Leu Arg Gln Val Asn Gln Ser Lys Val Gln Val Val Val
1179               260                   265                   270
1180 ctg ttt gcc tct gcc cgt gct gtc tac tcc ctt ttt agt tac agc atc 864
1181 Leu Phe Ala Ser Ala Arg Ala Val Tyr Ser Leu Phe Ser Tyr Ser Ile
1182          275                   280                   285
1183 cat cat ggc ctc tca ccc aag gta tgg gtg gcc agt gag tct tgg ctg 912
1184 His His Gly Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ser Trp Leu
1185      290                   295                   300
1186 aca tct gac ctg gtc atg aca ctt ccc aat att gcc cgt gtg ggc act 960
1187 Thr Ser Asp Leu Val Met Thr Leu Pro Asn Ile Ala Arg Val Gly Thr
1188 305                   310                   315                   320
1189 gtg ctt ggg ttt ttg cag cgg ggt gcc cta ctg cct gaa ttt tcc cat 1008
1190 Val Leu Gly Phe Leu Gln Arg Gly Ala Leu Leu Pro Glu Phe Ser His
1191                   325                   330                   335
```

```
1192 tat gtg gag act cac ctt gcc ctg gcc gct gac cca gca ttc tgt gcc 1056
1193 Tyr Val Glu Thr His Leu Ala Leu Ala Ala Asp Pro Ala Phe Cys Ala
1194         340             345             350
1195 tca ctg aat gcg gag ttg gat ctg gag gaa cat gtg atg ggg caa cgc 1104
1196 Ser Leu Asn Ala Glu Leu Asp Leu Glu Glu His Val Met Gly Gln Arg
1197         355             360             365
1198 tgt cca cgg tgt gac gac atc atg ctg cag aac cta tca tct ggg ctg 1152
1199 Cys Pro Arg Cys Asp Asp Ile Met Leu Gln Asn Leu Ser Ser Gly Leu
1200         370             375             380
1201 ttg cag aac cta tca gct ggg caa ttg cac cac caa ata ttt gca acc 1200
1202 Leu Gln Asn Leu Ser Ala Gly Gln Leu His His Gln Ile Phe Ala Thr
1203 385             390             395             400
1204 tat gca gct gtg tac agt gtg gct caa gcc ctt cac aac acc cta cag 1248
1205 Tyr Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln
1206         405             410             415
1207 tgc aat gtc tca cat tgc cac gta tca gaa cat gtt cta ccc tgg cag 1296
1208 Cys Asn Val Ser His Cys His Val Ser Glu His Val Leu Pro Trp Gln
1209         420             425             430
1210 ctc ctg gag aac atg tac aat atg agt ttc cat gct cga gac ttg aca 1344
1211 Leu Leu Glu Asn Met Tyr Asn Met Ser Phe His Ala Arg Asp Leu Thr
1212         435             440             445
1213 cta cag ttt gat gct gaa ggg aat gta gac atg gaa tat gac ctg aag 1392
1214 Leu Gln Phe Asp Ala Glu Gly Asn Val Asp Met Glu Tyr Asp Leu Lys
1215         450             455             460
1216 atg tgg gtg tgg cag agc cct aca cct gta tta cat act gtg ggc acc 1440
1217 Met Trp Val Trp Gln Ser Pro Thr Pro Val Leu His Thr Val Gly Thr
1218 465             470             475             480
1219 ttc aac ggc acc ctt cag ctg cag cag tct aaa atg tac tgg cca ggc 1488
1220 Phe Asn Gly Thr Leu Gln Leu Gln Gln Ser Lys Met Tyr Trp Pro Gly
1221         485             490             495
1222 aac cag gtg cca gtc tcc cag tgt tcc cgc cag tgc aaa gat ggc cag 1536
1223 Asn Gln Val Pro Val Ser Gln Cys Ser Arg Gln Cys Lys Asp Gly Gln
1224         500             505             510
1225 gtt cgc cga gta aag ggc ttt cat tcc tgc tgc tat gac tgc gtg gac 1584
1226 Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val Asp
1227         515             520             525
1228 tgc aag gcg ggc agc tac cgg aag cat cca gat gac ttc acc tgt act 1632
1229 Cys Lys Ala Gly Ser Tyr Arg Lys His Pro Asp Asp Phe Thr Cys Thr
1230         530             535             540
1231 cca tgt aac cag gac cag tgg tcc cca gag aaa agc aca gcc tgc tta 1680
1232 Pro Cys Asn Gln Asp Gln Trp Ser Pro Glu Lys Ser Thr Ala Cys Leu
1233 545             550             555             560
1234 cct cgc agg ccc aag ttt ctg gct tgg ggg gag cca gtt gtg ctg tca 1728
1235 Pro Arg Arg Pro Lys Phe Leu Ala Trp Gly Glu Pro Val Val Leu Ser
1236         565             570             575
1237 ctc ctc ctg ctg ctt tgc ctg gtg ctg ggt cta gca ctg gct gct ctg 1776
1238 Leu Leu Leu Leu Leu Cys Leu Val Leu Gly Leu Ala Leu Ala Ala Leu
1239         580             585             590
1240 ggg ctc tct gtc cac cac tgg gac agc cct ctt gtc cag gcc tca ggt 1824
```

```
1241 Gly Leu Ser Val His His Trp Asp Ser Pro Leu Val Gln Ala Ser Gly
1242         595             600             605
1243 ggc tca cag ttc tgc ttt ggc ctg atc tgc cta ggc ctc ttc tgc ctc 1872
1244 Gly Ser Gln Phe Cys Phe Gly Leu Ile Cys Leu Gly Leu Phe Cys Leu
1245     610             615             620
1246 agt gtc ctt ctg ttc cca ggg cgg cca agc tct gcc agc tgc ctt gca 1920
1247 Ser Val Leu Leu Phe Pro Gly Arg Pro Ser Ser Ala Ser Cys Leu Ala
1248 625             630             635             640
1249 caa caa cca atg gct cac ctc cct ctc aca ggc tgc ctg agc aca ctc 1968
1250 Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu
1251             645             ·650            655
1252 ttc ctg caa gca gct gag acc ttt gtg gag tct gag ctg cca ctg agc 2016
1253 Phe Leu Gln Ala Ala Glu Thr Phe Val Glu Ser Glu Leu Pro Leu Ser
1254             660             665             670
1255 tgg gca aac tgg cta tgc agc tac ctt cgg gga ctc tgg gcc tgg cta 2064
1256 Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Leu Trp Ala Trp Leu
1257         675             680             685
1258 gtg gta ctg ttg gcc act ttt gtg gag gca gca cta tgt gcc tgg tat 2112
1259 Val Val Leu Leu Ala Thr Phe Val Glu Ala Ala Leu Cys Ala Trp Tyr
1260     690             695             700
1261 ttg aac gct ttc cca cca gag gtg gtg aca gac tgg tca gtg ctg ccc 2160
1262 Leu Asn Ala Phe Pro Pro Glu Val Val Thr Asp Trp Ser Val Leu Pro
1263 705             710             715             720
1264 aca gag gta ctg gag cac tgc cac gtg cgt tcc tgg gtc agc ctg ggc 2208
1265 Thr Glu Val Leu Glu His Cys His Val Arg Ser Trp Val Ser Leu Gly
1266             725             730             735
1267 ttg gtg cac atc acc aat gca atg tta gct ttc ctc tgc ttt ctg ggc 2256
1268 Leu Val His Ile Thr Asn Ala Met Leu Ala Phe Leu Cys Phe Leu Gly
1269             740             745             750
1270 act ttc ctg gta cag agc cag cct ggc cgc tac aac cgt gcc cgt ggt 2304
1271 Thr Phe Leu Val Gln Ser Gln Pro Gly Arg Tyr Asn Arg Ala Arg Gly
1272         755             760             765
1273 ctc acc ttc gcc atg cta gct tat ttc atc acc tgg gtc tct ttt gtg 2352
1274 Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe Val
1275     770             775             780
1276 ccc ctc ctg gcc aat gtg cag gtg gcc tac cag cca gct gtg cag atg 2400
1277 Pro Leu Leu Ala Asn Val Gln Val Ala Tyr Gln Pro Ala Val Gln Met
1278 785             790             795             800
1279 ggt gct atc cta gtc tgt gcc ctg ggc atc ctg gtc acc ttc cac ctg 2448
1280 Gly Ala Ile Leu Val Cys Ala Leu Gly Ile Leu Val Thr Phe His Leu
1281             805             810             815
1282 ccc aag tgc tat gtg ctt ctt tgg ctg cca aag ctc aac acc cag gag 2496
1283 Pro Lys Cys Tyr Val Leu Leu Trp Leu Pro Lys Leu Asn Thr Gln Glu
1284             820             825             830
1285 ttc ttc ctg gga agg aat gcc aag aaa gca gca gat gag aac agt ggc 2544
1286 Phe Phe Leu Gly Arg Asn Ala Lys Lys Ala Ala Asp Glu Asn Ser Gly
1287         835             840             845
E--> 1288 ggt ggt gag gca gct cag gga cac aat gaa tga
1289 Gly Gly Glu Ala Ala Gln Gly His Asn Glu
```

2577 ← insert

```
        1290      850                  855
        1292 <210> SEQ ID NO: 19
        1293 <211> LENGTH: 29                      P.22
        1294 <212> TYPE: DNA
        1295 <213> ORGANISM: Artificial Sequence
W--> 1297 <220> FEATURE:
W--> 1297 <223> OTHER INFORMATION:
W--> 1297 <400> 19                               29 <- insert
E--> 1298 ggaattcatg cttttctggg cagctcacc
        1300 <210> SEQ ID NO: 20
        1301 <211> LENGTH: 38                      P.22
        1302 <212> TYPE: DNA
        1303 <213> ORGANISM: Artificial Sequence
W--> 1305 <220> FEATURE:
W--> 1305 <223> OTHER INFORMATION:
W--> 1305 <400> 20                               38 <- insert
E--> 1306 gcattacgat gcggccgctc aggtagtgcc gcagcgcc
        1308 <210> SEQ ID NO: 21
        1309 <211> LENGTH: 27                      P.22
        1310 <212> TYPE: DNA
        1311 <213> ORGANISM: Artificial Sequence
W--> 1313 <220> FEATURE:
W--> 1313 <223> OTHER INFORMATION:
W--> 1313 <400> 21                               27 <- insert
E--> 1314 ggaattcatg ggaccccagg cgaggac
        1316 <210> SEQ ID NO: 22
        1317 <211> LENGTH: 40                      P.22
        1318 <212> TYPE: DNA
        1319 <213> ORGANISM: Artificial Sequence
W--> 1321 <220> FEATURE:
W--> 1321 <223> OTHER INFORMATION:
W--> 1321 <400> 22                               40 <- insert
E--> 1322 gcattacgat gcggccgcct agctcttcct catcgtgtag
        1324 <210> SEQ ID NO: 23
        1325 <211> LENGTH: 29                      P.22
        1326 <212> TYPE: DNA
        1327 <213> ORGANISM: Artificial Sequence
W--> 1329 <220> FEATURE:
W--> 1329 <223> OTHER INFORMATION:
W--> 1329 <400> 23                               29 <- insert
E--> 1330 ggaattcatg ccagctttgg ctatcatgg
        1332 <210> SEQ ID NO: 24
        1333 <211> LENGTH: 41                      P.22
        1334 <212> TYPE: DNA
        1335 <213> ORGANISM: Artificial Sequence
W--> 1337 <220> FEATURE:
W--> 1337 <223> OTHER INFORMATION:
W--> 1337 <400> 24                               41 <- insert
E--> 1338 gcattacgat gcggccgctc attcattgtg ttcctgagct g
```

delete

E--> 1339 (1)
E--> 1342 (1)

RAW SEQUENCE LISTING   DATE: 07/06/2004
PATENT APPLICATION: **US/10/663,650**   TIME: 15:31:24

Input Set : **A:\US-972-Sequence.txt**
Output Set: **N:\CRF4\07062004\J663650.raw**

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 07/06/2004
PATENT APPLICATION: US/10/663,650 TIME: 15:31:25

Input Set : **A:\US-972-Sequence.txt**
Output Set: **N:\CRF4\07062004\J663650.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:4; Line(s) 186
Seq#:15; Line(s) 706

Use of <220> Feature(NEW RULES): *error explanation*
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:4,7,8,11,12,13,14,15,19,20,21,22,23,24

VERIFICATION SUMMARY   DATE: 07/06/2004
PATENT APPLICATION: **US/10/663,650**   TIME: 15:31:25

Input Set : **A:\US-972-Sequence.txt**
Output Set: **N:\CRF4\07062004\J663650.raw**

```
L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE
L:5 M:283 W: Missing Blank Line separator, <160> field identifier
L:15 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:1
L:73 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:2
L:131 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:3
L:192 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:192 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:192 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:192
L:365 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:6
L:443 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1353 SEQ:6
L:450 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:450 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:7, <213>
ORGANISM:Artificial Sequence
L:450 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:450
L:451 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:7
L:458 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:458 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:458 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:458
L:459 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:37 SEQ:8
L:469 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:9
L:469 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:9 differs:8
L:501 M:254 E: No. of Bases conflict, LENGTH:Input:669 Counted:699 SEQ:9
L:567 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:10
L:665 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2679 SEQ:10
L:672 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:672 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>
ORGANISM:Artificial Sequence
L:672 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:672
L:673 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:11
L:680 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial Sequence
L:680 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial Sequence
L:680 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:680
L:681 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:12
L:688 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:688 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:688 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:688
L:689 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:13
L:696 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:696 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
```

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ORGANISM:Artificial Sequence
L:696 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:696
L:697 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:37 SEQ:14
L:711 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:711 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:711 M:283 W: Missing Blank Line separator, <400> field identifier
L:711 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:711
L:781 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1122 SEQ:15
L:793 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:16
```

VERIFICATION SUMMARY   DATE: 07/06/2004
PATENT APPLICATION: **US/10/663,650**   TIME: 15:31:25

Input Set : **A:\US-972-Sequence.txt**
Output Set: **N:\CRF4\07062004\J663650.raw**

L:950 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2529 SEQ:16
L:962 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:17
L:1119 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2532 SEQ:17
L:1288 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:2577 SEQ:18
L:1297 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:1297 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:1297 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:1297
L:1298 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:19
L:1305 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:1305 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:1305 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:1305
L:1306 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:38 SEQ:20
L:1313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:1313 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:1313 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:1313
L:1314 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:21
L:1321 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:1321 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:22, <213>
ORGANISM:Artificial Sequence
L:1321 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:22,Line#:1321
L:1322 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:22
L:1329 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:1329 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:1329 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1329
L:1330 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:23
L:1337 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:1337 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:1337 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:1337
L:1338 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:24
M:254 Repeated in SeqNo=24